

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Patent Application of:
Markus Matuschek et al.

Application No.: 10/521,916

Confirmation No.: N/A

Filed: January 20, 2005

Art Unit: N/A

For: PROCESS FOR THE BIOTRANSFORMATION
OF CAROTENOIDS

Examiner: Not Yet Assigned

**STATEMENT TO SUPPORT FILING AND SUBMISSION
IN ACCORDANCE WITH 37 CFR §§1.821 THROUGH 1.825**

MS Sequence
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Dear Sir:

- I hereby state, in accordance with the requirements of 37 C.F.R. §1.821(f), that the information recorded in computer readable form is identical to the written Sequence Listing submitted herewith.
- I hereby state that the submission filed in accordance with 37 C.F.R. 1.821(g) does not include new matter.
- I hereby state that the submission filed in accordance with 37 C.F.R. §1.821(h) does not include new matter or go beyond the disclosure in the international application as filed.
- I hereby state that the amendments, made in accordance with 37 C.F.R. §1.825(a), included in the substitute sheet(s) of the Sequence Listing are supported in the application, as filed, in pages 1-11 of the Sequence Listing. I hereby state that the substitute sheets of the Sequence Listing do not include new matter.
- I hereby state that the substitute copy of the computer readable form, submitted in accordance with 37 C.F.R. §1.825(b), is the same as the amended Sequence Listing.
- I hereby state that the substitute copy of the computer readable form, submitted in accordance with 37 C.F.R. §1.825(d), contains identical data to that originally filed on January 20, 2005.

Dated: *April 26, 2005*

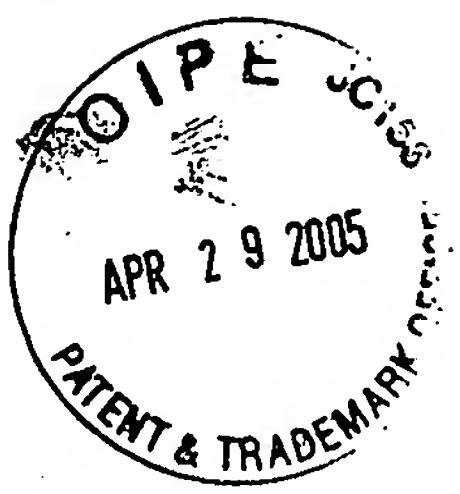
Respectfully submitted,

By Christine M. Hansen

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10/521916

SEQUENCE LISTING

<110> Matuschek, Markus

Hauer, Bernhard

Schmid, Rolf

Kauffmann, Isabelle

Blasco, Francesca

Schmidt-Dannert, Claudia

<120> Process for the biotransformation of carotenoids

<130> 13111-00001-US

<140> 10/521,916

<141> 2005-01-20

<150> PCT/EP2003/008199

<151> 2003-07-25

<150> DE 102 34 126.5

<151> 2002-07-26

<160> 12

<170> PatentIn Ver. 3.3

<210> 1

<211> 1170

<212> DNA

<213> Thermus thermophilus

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<221> CDS

<222> (1) .. (1170)

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atg aag cgc ctt tcc ctg agg gag gcc tgg ccc tac ctg aaa gac ctc 48
Met Lys Arg Leu Ser Leu Arg Glu Ala Trp Pro Tyr Leu Lys Asp Leu
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cag caa gat ccc ctc gcc gtc ctg ctg gcg tgg ggc cg^g gcc cac ccc 96
Gln Gln Asp Pro Leu Ala Val Leu Leu Ala Trp Gly Arg Ala His Pro
20 25 30

cg^g ctc ttc ctt ccc ctg ccc cgc ttc ccc ctg gcc ctg atc ttt gac 144
Arg Leu Phe Leu Pro Leu Pro Arg Phe Pro Leu Ala Leu Ile Phe Asp
35 40 45

ccc gag ggg gtg gag ggg gcg ctc ctc gcc gag ggg acc acc aag gcc 192
Pro Glu Gly Val Glu Gly Ala Leu Leu Ala Glu Gly Thr Thr Lys Ala
50 55 60

acc ttc cag tac cg _g gcc ctc tcc cgc ctc acg ggg agg ggc ctc ctc	240
Thr Phe Gln Tyr Arg Ala Leu Ser Arg Leu Thr Gly Arg Gly Leu Leu	
65 70 75 80	
acc gac tgg ggg gaa agc tgg aag gag gc _g cgc aag gcc ctc aaa gac	288
Thr Asp Trp Gly Glu Ser Trp Lys Glu Ala Arg Lys Ala Leu Lys Asp	
85 90 95	
ccc ttc ctg cc _g aag aac gtc cgc ggc tac cg _g gag gcc atg gag gag	336
Pro Phe Leu Pro Lys Asn Val Arg Gly Tyr Arg Glu Ala Met Glu Glu	
100 105 110	
gag gcc cg _g gcc ttc ttc ggg gag tgg cg _g ggg gag gag cg _g gac ct _g	384
Glu Ala Arg Ala Phe Phe Gly Glu Trp Arg Gly Glu Glu Arg Asp Leu	
115 120 125	
gac cac gag atg ctc gcc ctc tcc ctg cgc ctc ctc ggg cg _g gcc ctc	432
Asp His Glu Met Leu Ala Leu Ser Leu Arg Leu Leu Gly Arg Ala Leu	
130 135 140	
ttc ggg aag ccc ctc tcc cca agc ctc gc _g gag cac gcc ctt aag gcc	480
Phe Gly Lys Pro Leu Ser Pro Ser Leu Ala Glu His Ala Leu Lys Ala	
145 150 155 160	
ctg gac cg _g atc atg gcc cag acc agg agc ccc ctg gcc ctc ctg gac	528
Leu Asp Arg Ile Met Ala Gln Thr Arg Ser Pro Leu Ala Leu Leu Asp	
165 170 175	
ctg gcc gaa gcc cg _g ttc cg _g aag gac cg _g ggg gcc ctc tac cg _g	576
Leu Ala Ala Glu Ala Arg Phe Arg Lys Asp Arg Gly Ala Leu Tyr Arg	
180 185 190	
gag gc _g gaa gcc ctc atc gtc cac cc _g ccc ctc tcc cac ctt ccc cga	624
Glu Ala Glu Ala Leu Ile Val His Pro Pro Leu Ser His Leu Pro Arg	
195 200 205	
gag cg _g gcc ctg agc gag gc _g gt _g acc ctc ctg gt _g gc _g ggc cac gag	672
Glu Arg Ala Leu Ser Glu Ala Val Thr Leu Leu Val Ala Gly His Glu	
210 215 220	
ac _g gt _g gc _g agc gc _g ctc acc tgg tcc ttt ctc ctc ctc tcc cac cg _g	720
Thr Val Ala Ser Ala Leu Thr Trp Ser Phe Leu Leu Leu Ser His Arg	
225 230 235 240	
cc _g gac tgg cag aag cg _g gt _g gcc gag agc gag gag gc _g gcc ctc gc _g	768
Pro Asp Trp Gln Lys Arg Val Ala Glu Ser Glu Glu Ala Ala Leu Ala	
245 250 255	
gcc ttc cag gag gc _g ctg agg ctc tac cc _g ccc gcc tgg atc ctc acc	816
Ala Phe Gln Glu Ala Leu Arg Leu Tyr Pro Pro Ala Trp Ile Leu Thr	
260 265 270	
cg _g agg ctg gaa agg cc _g ctc ctc ctg gga gag gac cg _g ctc ccc cc _g	864
Arg Arg Leu Glu Arg Pro Leu Leu Leu Gly Glu Asp Arg Leu Pro Pro	
275 280 285	
ggc acc acc ctg gtc ctc tcc ccc tac gt _g acc cag agg ctc cac tt _c	912

Gly Thr Thr Leu Val Leu Ser Pro Tyr Val Thr Gln Arg Leu His Phe				
290	295	300		
ccc gat ggg gag gcc ttc cgg ccc gag cgc ttc ctg gag gaa agg ggg				960
Pro Asp Gly Glu Ala Phe Arg Pro Glu Arg Phe Leu Glu Glu Arg Gly				
305	310	315	320	
acc cct tcg ggg cgc tac ttc ccc ttt ggc ctg ggg cag agg ctc tgc				1008
Thr Pro Ser Gly Arg Tyr Phe Pro Phe Gly Leu Gly Gln Arg Leu Cys				
325	330	335		
ctg ggg cgg gac ttc gcc ctc ctc gag ggc ccc atc gtc ctc agg gcc				1056
Leu Gly Arg Asp Phe Ala Leu Leu Glu Gly Pro Ile Val Leu Arg Ala				
340	345	350		
tcc ttc cgc cgc ttc cgc cta gac ccc ctc ccc ttc ccc cgg gtc ctc				1104
Phe Phe Arg Arg Phe Arg Leu Asp Pro Leu Pro Phe Pro Arg Val Leu				
355	360	365		
gcc cag gtc acc ctg agg ccc gaa ggc ggg ctt ccc gcg cgg cct agg				1152
Ala Gln Val Thr Leu Arg Pro Glu Gly Leu Pro Ala Arg Pro Arg				
370	375	380		
gag gag gtg cgg gcg tga				1170
Glu Glu Val Arg Ala				
385				
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20	25	30		
Arg Leu Phe Leu Pro Leu Pro Arg Phe Pro Leu Ala Leu Ile Phe Asp				
35	40	45		
Pro Glu Gly Val Glu Gly Ala Leu Leu Ala Glu Gly Thr Thr Lys Ala				
50	55	60		
Thr Phe Gln Tyr Arg Ala Leu Ser Arg Leu Thr Gly Arg Gly Leu Leu				
65	70	75	80	
Thr Asp Trp Gly Glu Ser Trp Lys Glu Ala Arg Lys Ala Leu Lys Asp				
85	90	95		
Pro Phe Leu Pro Lys Asn Val Arg Gly Tyr Arg Glu Ala Met Glu Glu				
100	105	110		

Glu Ala Arg Ala Phe Phe Gly Glu Trp Arg Gly Glu Glu Arg Asp Leu
 115 120 125

Asp His Glu Met Leu Ala Leu Ser Leu Arg Leu Leu Gly Arg Ala Leu
 130 135 140

Phe Gly Lys Pro Leu Ser Pro Ser Leu Ala Glu His Ala Leu Lys Ala
 145 150 155 160

Leu Asp Arg Ile Met Ala Gln Thr Arg Ser Pro Leu Ala Leu Leu Asp
 165 170 175

Leu Ala Ala Glu Ala Arg Phe Arg Lys Asp Arg Gly Ala Leu Tyr Arg
 180 185 190

Glu Ala Glu Ala Leu Ile Val His Pro Pro Leu Ser His Leu Pro Arg
 195 200 205

Glu Arg Ala Leu Ser Glu Ala Val Thr Leu Leu Val Ala Gly His Glu
 210 215 220

Thr Val Ala Ser Ala Leu Thr Trp Ser Phe Leu Leu Leu Ser His Arg
 225 230 235 240

Pro Asp Trp Gln Lys Arg Val Ala Glu Ser Glu Glu Ala Ala Leu Ala
 245 250 255

Ala Phe Gln Glu Ala Leu Arg Leu Tyr Pro Pro Ala Trp Ile Leu Thr
 260 265 270

Arg Arg Leu Glu Arg Pro Leu Leu Gly Glu Asp Arg Leu Pro Pro
 275 280 285

Gly Thr Thr Leu Val Leu Ser Pro Tyr Val Thr Gln Arg Leu His Phe
 290 295 300

Pro Asp Gly Glu Ala Phe Arg Pro Glu Arg Phe Leu Glu Glu Arg Gly
 305 310 315 320

Thr Pro Ser Gly Arg Tyr Phe Pro Phe Gly Leu Gly Gln Arg Leu Cys
 325 330 335

Leu Gly Arg Asp Phe Ala Leu Leu Glu Gly Pro Ile Val Leu Arg Ala
 340 345 350

Phe Phe Arg Arg Phe Arg Leu Asp Pro Leu Pro Phe Pro Arg Val Leu
 355 360 365

Ala Gln Val Thr Leu Arg Pro Glu Gly Gly Leu Pro Ala Arg Pro Arg
 370 375 380

Glu Glu Val Arg Ala
 385

<211> 1188

<212> DNA

<213> Artificial sequence

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<221> misc_feature

<222> (4)..(21)

<223> His tag

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<223> Description of the artificial sequence: N-terminal
his tagged

<220>

<221> CDS

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ccc tac ctg aaa gac ctc cag caa gat ccc ctc gcc gtc ctg ctg gcg	96
Pro Tyr Leu Lys Asp Leu Gln Gln Asp Pro Leu Ala Val Leu Leu Ala	
20 25 30	

tgg ggc cg ^g gcc cac ccc cg ^g ctc ttc ctt ccc ctg ccc cgc ttc ccc	144
Trp Gly Arg Ala His Pro Arg Leu Phe Leu Pro Leu Pro Arg Phe Pro	
35 40 45	

ctg gcc ctg atc ttt gac ccc gag ggg gtg gag ggg gcg ctc ctc gcc	192
Leu Ala Leu Ile Phe Asp Pro Glu Gly Val Glu Gly Ala Leu Leu Ala	
50 55 60	

gag ggg acc acc aag gcc acc ttc cag tac cg ^g gcc ctc tcc cgc ctc	240
Glu Gly Thr Thr Lys Ala Thr Phe Gln Tyr Arg Ala Leu Ser Arg Leu	
65 70 75 80	

acg ggg agg ggc ctc ctc acc gac tgg ggg gaa agc tgg aag gag gcg	288
Thr Gly Arg Gly Leu Leu Thr Asp Trp Gly Glu Ser Trp Lys Glu Ala	
85 90 95	

cgc aag gcc ctc aaa gac ccc ttc ctg ccg aag aac gtc cgc ggc tac	336
Arg Lys Ala Leu Lys Asp Pro Phe Leu Pro Lys Asn Val Arg Gly Tyr	
100 105 110	

cgg gag gcc atg gag gag gcc cg ^g gcc ttc ttc ggg gag tgg cg ^g	384
Arg Glu Ala Met Glu Glu Ala Arg Ala Phe Phe Gly Glu Trp Arg	

115	120	125	
ggg gag gag cg ^g gac ctg gac cac gag atg ctc gcc ctc tcc ctg cgc Gly Glu Glu Arg Asp Leu Asp His Glu Met Leu Ala Leu Ser Leu Arg 130	135	140	432
ctc ctc ggg cg ^g gcc ctc ttc ggg aag ccc ctc tcc cca agc ctc gcg Leu Leu Gly Arg Ala Leu Phe Gly Lys Pro Leu Ser Pro Ser Leu Ala 145	150	155	480
gag cac gcc ctt aag gcc ctg gac cg ^g atc atg gcc cag acc agg agc Glu His Ala Leu Lys Ala Leu Asp Arg Ile Met Ala Gln Thr Arg Ser 165	170	175	528
ccc ctg gcc ctc ctg gac ctg gcc gaa gcc cg ^c ttc cg ^g aag gac Pro Leu Ala Leu Leu Asp Leu Ala Ala Glu Ala Arg Phe Arg Lys Asp 180	185	190	576
cg ^g ggg gcc ctc tac cg ^c gag gc ^g gaa gcc ctc atc gtc cac cc ^g ccc Arg Gly Ala Leu Tyr Arg Glu Ala Glu Ala Leu Ile Val His Pro Pro 195	200	205	624
ctc tcc cac ctt ccc cga gag cg ^c gcc ctg agc gag gcc gt ^g acc ctc Leu Ser His Leu Pro Arg Glu Arg Ala Leu Ser Glu Ala Val Thr Leu 210	215	220	672
ctg gt ^g gc ^g gg ^c cac gag acg gt ^g gc ^g agc gcc ctc acc tgg tcc ttt Leu Val Ala Gly His Glu Thr Val Ala Ser Ala Leu Thr Trp Ser Phe 225	230	235	720
ctc ctc ctc tcc cac cg ^c cc ^g gac tgg cag aag cg ^g gt ^g gcc gag agc Leu Leu Leu Ser His Arg Pro Asp Trp Gln Lys Arg Val Ala Glu Ser 245	250	255	768
gag gag gc ^g gcc ctc gcc ttc cag gag gc ^g ctg agg ctc tac cc ^c Glu Glu Ala Ala Leu Ala Ala Phe Gln Glu Ala Leu Arg Leu Tyr Pro 260	265	270	816
ccc gcc tgg atc ctc acc cg ^g agg ctg gaa agg ccc ctc ctc ctg gga Pro Ala Trp Ile Leu Thr Arg Arg Leu Glu Arg Pro Leu Leu Leu Gly 275	280	285	864
gag gac cg ^g ctc ccc cc ^g gg ^c acc acc ctg gtc ctc tcc cc ^c tac gt ^g Glu Asp Arg Leu Pro Pro Gly Thr Thr Leu Val Leu Ser Pro Tyr Val 290	295	300	912
acc cag agg ctc cac ttc cc ^c gat gg ^g gag gc ^g ttc cg ^g cc ^c gag cg ^c Thr Gln Arg Leu His Phe Pro Asp Gly Glu Ala Phe Arg Pro Glu Arg 305	310	315	960
t ^t c ctg gag gaa agg gg ^g acc cct tc ^t gg ^g cg ^c tac tt ^t cc ^c tt ^t gg ^c Phe Leu Glu Glu Arg Gly Thr Pro Ser Gly Arg Tyr Phe Pro Phe Gly 325	330	335	1008
ctg ggg cag agg ctc tgc ctg gg ^g cg ^g gac tt ^t gc ^g ctc ctc gag gg ^c Leu Gly Gln Arg Leu Cys Leu Gly Arg Asp Phe Ala Leu Leu Glu Gly 340	345	350	1056

ccc atc gtc ctc agg gcc ttc ttc cgc cgc ttc cgc cta gac ccc ctc 1104
 Pro Ile Val Leu Arg Ala Phe Phe Arg Arg Phe Arg Leu Asp Pro Leu
 355 360 365

ccc ttc ccc cggtc ctc gcc cag gtc acc ctg agg ccc gaa ggc ggg 1152
 Pro Phe Pro Arg Val Leu Ala Gln Val Thr Leu Arg Pro Glu Gly Gly
 370 375 380

ctt ccc gcg cggtc cct agg gag gag gtg cggtc gcg tga 1188
 Leu Pro Ala Arg Pro Arg Glu Glu Val Arg Ala
 385 390 395

<210> 4

<211> 395

<212> PRT

<213> Artificial sequence

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<223> Description of the artificial sequence: N-terminal
 his tagged

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 1 5 10 15

Pro Tyr Leu Lys Asp Leu Gln Gln Asp Pro Leu Ala Val Leu Leu Ala
 20 25 30

Trp Gly Arg Ala His Pro Arg Leu Phe Leu Pro Leu Pro Arg Phe Pro
 35 40 45

Leu Ala Leu Ile Phe Asp Pro Glu Gly Val Glu Gly Ala Leu Leu Ala
 50 55 60

Glu Gly Thr Thr Lys Ala Thr Phe Gln Tyr Arg Ala Leu Ser Arg Leu
 65 70 75 80

Thr Gly Arg Gly Leu Leu Thr Asp Trp Gly Glu Ser Trp Lys Glu Ala
 85 90 95

Arg Lys Ala Leu Lys Asp Pro Phe Leu Pro Lys Asn Val Arg Gly Tyr
 100 105 110

Arg Glu Ala Met Glu Glu Ala Arg Ala Phe Phe Gly Glu Trp Arg
 115 120 125

Gly Glu Glu Arg Asp Leu Asp His Glu Met Leu Ala Leu Ser Leu Arg
 130 135 140

Leu Leu Gly Arg Ala Leu Phe Gly Lys Pro Leu Ser Pro Ser Leu Ala
 145 150 155 160

Glu His Ala Leu Lys Ala Leu Asp Arg Ile Met Ala Gln Thr Arg Ser
 165 170 175

 Pro Leu Ala Leu Leu Asp Leu Ala Ala Glu Ala Arg Phe Arg Lys Asp
 180 185 190

 Arg Gly Ala Leu Tyr Arg Glu Ala Glu Ala Leu Ile Val His Pro Pro
 195 200 205

 Leu Ser His Leu Pro Arg Glu Arg Ala Leu Ser Glu Ala Val Thr Leu
 210 215 220

 Leu Val Ala Gly His Glu Thr Val Ala Ser Ala Leu Thr Trp Ser Phe
 225 230 235 240

 Leu Leu Leu Ser His Arg Pro Asp Trp Gln Lys Arg Val Ala Glu Ser
 245 250 255

 Glu Glu Ala Ala Leu Ala Ala Phe Gln Glu Ala Leu Arg Leu Tyr Pro
 260 265 270

 Pro Ala Trp Ile Leu Thr Arg Arg Leu Glu Arg Pro Leu Leu Leu Gly
 275 280 285

 Glu Asp Arg Leu Pro Pro Gly Thr Thr Leu Val Leu Ser Pro Tyr Val
 290 295 300

 Thr Gln Arg Leu His Phe Pro Asp Gly Glu Ala Phe Arg Pro Glu Arg
 305 310 315 320

 Phe Leu Glu Glu Arg Gly Thr Pro Ser Gly Arg Tyr Phe Pro Phe Gly
 325 330 335

 Leu Gly Gln Arg Leu Cys Leu Gly Arg Asp Phe Ala Leu Leu Glu Gly
 340 345 350

 Pro Ile Val Leu Arg Ala Phe Phe Arg Arg Phe Arg Leu Asp Pro Leu
 355 360 365

 Pro Phe Pro Arg Val Leu Ala Gln Val Thr Leu Arg Pro Glu Gly Gly
 370 375 380

 Leu Pro Ala Arg Pro Arg Glu Glu Val Arg Ala
 385 390 395

<210> 5

<211> 1188

<212> DNA

<213> Artificial sequence

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<221> misc_feature

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<223> His tag

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<223> Description of the artificial sequence: N-terminal
His-tagged

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<221> CDS

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1 5	10	15

cag caa gat ccc ctc gcc gtc ctg ctg gcg tgg ggc	cgg gcc cac ccc	96
Gln Gln Asp Pro Leu Ala Val Leu Ala Trp Gly Arg	Ala His Pro	
20 25	30	

cgg ctc ttc ctt ccc ctg ccc cgc ttc ccc ctg gcc	ctg atc ttt gac	144
Arg Leu Phe Leu Pro Leu Pro Arg Phe Pro Leu Ala	Ile Leu Phe Asp	
35 40	45	

ccc gag ggg gtg gag ggg gcg ctc ctc gcc gag	ggg acc acc aag gcc	192
Pro Glu Gly Val Glu Gly Ala Leu Leu Ala Glu	Gly Thr Thr Lys Ala	
50 55	60	

acc ttc cag tac cgg gcc ctc tcc cgc ctc acg	ggg agg ggc ctc ctc	240
Thr Phe Gln Tyr Arg Ala Leu Ser Arg Leu Thr	Gly Arg Gly Leu Leu	
65 70	75 80	

acc gac tgg ggg gaa agc tgg aag gag gcg	cgc aag gcc ctc aaa gac	288
Thr Asp Trp Gly Glu Ser Trp Lys Glu Ala Arg	Lys Ala Leu Lys Asp	
85 90	95	

ccc ttc ctg ccg aag aac gtc cgc ggc tac	cgg gag gcc atg gag gag	336
Pro Phe Leu Pro Lys Asn Val Arg Gly Tyr Arg	Glu Ala Met Glu Glu	
100 105	110	

gag gcc cggttccgggggagttggcgggggag	gag cggttccgggggag	384
Glu Ala Arg Ala Phe Phe Gly Glu Trp Arg Gly	Glu Glu Arg Asp Leu	
115 120	125	

gac cac gag atg ctc gcc ctc tcc ctg cgc ctc	ctc ggg cggttccgggggag	432
Asp His Glu Met Leu Ala Leu Ser Leu Arg Leu	Gly Arg Ala Leu	
130 135	140	

ttc ggg aag ccc ctc tcc cca agc ctc gcg	gag cac gcc ctt aag gcc	480
Phe Gly Lys Pro Leu Ser Pro Ser Leu Ala Glu	His Ala Leu Lys Ala	

145	150	155	160	
ctg gac cg	atc atg gcc cag acc agg agc ccc ctg gcc ctc ctg gac			528
Leu Asp Arg Ile Met Ala Gln Thr Arg Ser Pro Leu Ala Leu Leu Asp				
165	170	175		
ctg gcc gcc gaa gcc cgc ttc cg	aag gac cg	ggg gcc ctc tac cgc		576
Leu Ala Ala Glu Ala Arg Phe Arg Lys Asp Arg Gly Ala Leu Tyr Arg				
180	185	190		
gag gcg gaa gcc ctc atc gtc cac ccg ccc ctc tcc cac ctt ccc cga				624
Glu Ala Glu Ala Leu Ile Val His Pro Pro Leu Ser His Leu Pro Arg				
195	200	205		
gag cgc gcc ctg agc gag gcc gtg acc ctc ctg gtg gcg ggc cac gag				672
Glu Arg Ala Leu Ser Glu Ala Val Thr Leu Leu Val Ala Gly His Glu				
210	215	220		
acg gtg gcg agc gcc ctc acc tgg tcc ttt ctc ctc ctc tcc cac cgc				720
Thr Val Ala Ser Ala Leu Thr Trp Ser Phe Leu Leu Leu Ser His Arg				
225	230	235	240	
ccg gac tgg cag aag cgg gtg gcc gag agc gag gag gcg gcc ctc gcc				768
Pro Asp Trp Gln Lys Arg Val Ala Glu Ser Glu Glu Ala Ala Leu Ala				
245	250	255		
gcc ttc cag gag gcc ctg agg ctc tac ccc ccc gcc tgg atc ctc acc				816
Ala Phe Gln Glu Ala Leu Arg Leu Tyr Pro Pro Ala Trp Ile Leu Thr				
260	265	270		
cgg agg ctg gaa agg ccc ctc ctc ctg gga gag gac cgg ctc ccc ccg				864
Arg Arg Leu Glu Arg Pro Leu Leu Leu Gly Glu Asp Arg Leu Pro Pro				
275	280	285		
ggc acc acc ctg gtc ctc tcc ccc tac gtg acc cag agg ctc cac ttc				912
Gly Thr Thr Leu Val Leu Ser Pro Tyr Val Thr Gln Arg Leu His Phe				
290	295	300		
ccc gat ggg gag gcc ttc cgg ccc gag cgc ttc ctg gag gaa agg ggg				960
Pro Asp Gly Glu Ala Phe Arg Pro Glu Arg Phe Leu Glu Glu Arg Gly				
305	310	315	320	
acc cct tcg ggg cgc tac ttc ccc ttt ggc ctg ggg cag agg ctc tgc				1008
Thr Pro Ser Gly Arg Tyr Phe Pro Phe Gly Leu Gly Gln Arg Leu Cys				
325	330	335		
ctg ggg cgg gac ttc gcc ctc ctc gag ggc ccc atc gtc ctc agg gcc				1056
Leu Gly Arg Asp Phe Ala Leu Leu Glu Gly Pro Ile Val Leu Arg Ala				
340	345	350		
ttc ttc cgc cgc ttc cgc cta gac ccc ctc ccc ttc ccc cgg gtc ctc				1104
Phe Phe Arg Arg Phe Arg Leu Asp Pro Leu Pro Phe Pro Arg Val Leu				
355	360	365		
gcc cag gtc acc ctg agg ccc gaa ggc ggg ctt ccc gcg cgg cct agg				1152
Ala Gln Val Thr Leu Arg Pro Glu Gly Gly Leu Pro Ala Arg Pro Arg				
370	375	380		

gag gag gtg cg^g g^c cat cac cat cat cat cac tga 1188
Glu Glu Val Arg Ala His His His His His
385 . 390 395

<210> 6

<211> 395

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: C-terminal His-tagged

<400> 6

Met Lys Arg Leu Ser Leu Arg Glu Ala Trp Pro Tyr Leu Lys Asp Leu
1 5 10 15

Gln Gln Asp Pro Leu Ala Val Leu Leu Ala Trp Gly Arg Ala His Pro
20 25 30

Arg Leu Phe Leu Pro Leu Pro Arg Phe Pro Leu Ala Leu Ile Phe Asp
35 40 45

Pro Glu Gly Val Glu Gly Ala Leu Leu Ala Glu Gly Thr Thr Lys Ala
50 55 60

Thr Phe Gln Tyr Arg Ala Leu Ser Arg Leu Thr Gly Arg Gly Leu Leu
65 70 75 80

Thr Asp Trp Gly Glu Ser Trp Lys Glu Ala Arg Lys Ala Leu Lys Asp
85 90 95

Pro Phe Leu Pro Lys Asn Val Arg Gly Tyr Arg Glu Ala Met Glu Glu
100 105 110

Glu Ala Arg Ala Phe Phe Gly Glu Trp Arg Gly Glu Glu Arg Asp Leu
115 120 125

Asp His Glu Met Leu Ala Leu Ser Leu Arg Leu Leu Gly Arg Ala Leu
130 135 140

Phe Gly Lys Pro Leu Ser Pro Ser Leu Ala Glu His Ala Leu Lys Ala
145 150 155 160

Leu Asp Arg Ile Met Ala Gln Thr Arg Ser Pro Leu Ala Leu Leu Asp
165 170 175

Leu Ala Ala Glu Ala Arg Phe Arg Lys Asp Arg Gly Ala Leu Tyr Arg
180 185 190

Glu Ala Glu Ala Leu Ile Val His Pro Pro Leu Ser His Leu Pro Arg

195	200	205
Glu Arg Ala Leu Ser Glu Ala Val Thr Leu Leu Val Ala Gly His Glu		
210	215	220
Thr Val Ala Ser Ala Leu Thr Trp Ser Phe Leu Leu Leu Ser His Arg		
225	230	235
240		
Pro Asp Trp Gln Lys Arg Val Ala Glu Ser Glu Glu Ala Ala Leu Ala		
245	250	255
Ala Phe Gln Glu Ala Leu Arg Leu Tyr Pro Pro Ala Trp Ile Leu Thr		
260	265	270
Arg Arg Leu Glu Arg Pro Leu Leu Leu Gly Glu Asp Arg Leu Pro Pro		
275	280	285
Gly Thr Thr Leu Val Leu Ser Pro Tyr Val Thr Gln Arg Leu His Phe		
290	295	300
Pro Asp Gly Glu Ala Phe Arg Pro Glu Arg Phe Leu Glu Glu Arg Gly		
305	310	315
320		
Thr Pro Ser Gly Arg Tyr Phe Pro Phe Gly Leu Gly Gln Arg Leu Cys		
325	330	335
Leu Gly Arg Asp Phe Ala Leu Leu Glu Gly Pro Ile Val Leu Arg Ala		
340	345	350
Phe Phe Arg Arg Phe Arg Leu Asp Pro Leu Pro Phe Pro Arg Val Leu		
355	360	365
Ala Gln Val Thr Leu Arg Pro Glu Gly Leu Pro Ala Arg Pro Arg		
370	375	380
Glu Glu Val Arg Ala His His His His His His		
385	390	395

<210> 7

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR primer

<400> 7

cgaagctcat atgaagcgcc tttccctgag

30

<210> 8

<211> 30
<212> DNA
<213> Artificial sequence
<220>
<223> Description of the artificial sequence: PCR primer

<400> 8
gcgaattcac gccccaccc cctccctagg 30

<210> 9
<211> 42
<212> DNA
<213> Artificial sequence
<220>
<223> Description of the artificial sequence: PCR primer

<400> 9
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<210> 10
<211> 42
<212> DNA
<213> Artificial sequence
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<223> Description of the artificial sequence: PCR primer

<400> 10
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<210> 11
<211> 30
<212> DNA
<213> Artificial sequence
<220>

<223> Description of the artificial sequence: PCR primer

<400> 11

ccggaattca tgaagcgctt ttccctgagg

30

<210> 12

<211> 44

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR primer

<400> 12

ccaatgcatt ggttctgcag tcaggccccgc acctcctccc tagg

44